

## SEQUENCE LISTING

&lt;110&gt; Hyseq, Inc.

<120> A NOVEL EGF MOTIF PROTEIN OBTAINED FROM  
A cDNA LIBRARY OF FETAL LIVER-SPLEEN

&lt;130&gt; 20411-720

&lt;140&gt; US 08/968,800

&lt;141&gt; 1997-11-22

&lt;160&gt; 20

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(300)

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(300)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 1

ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct 48  
 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro  
 1 5 10 15

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96  
 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe  
 20 25 30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144  
 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly  
 35 40 45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192  
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
 50 55 60

tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
65					70					75					80	

tgt	gtg	aac	tcn	agg	aca	tgt	gcc	atg	ata	aac	tgt	cag	tat	agc	tgt	288
Cys	Val	Asn	Xaa	Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	
				85					90					95		

gaa	gac	aca	gaa													300
Glu	Asp	Thr	Glu													
			100													

<210> 2  
 <211> 1611  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> CDS  
 <222> (1)...(1506)  
  
 <221> misc\_feature  
 <222> (1)...(1611)  
 <223> n = A,T,C or G

al  
cont

ggc	tgg	aga	aga	aac	agc	aag	gga	gtc	tgt	gaa	gct	aca	tgc	gaa	cct	48
Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	
1				5					10					15		

gga	tgt	aag	ttt	ggt	gag	tgc	gtg	gga	cca	aac	aaa	tgc	aga	tgc	ttt	96
Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	
			20					25					30			

cca	gga	tac	acc	ggg	aaa	acc	tgc	agt	caa	gat	gtg	aat	gag	tgt	gga	144
Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	
		35					40					45				

atg	aaa	ccc	cgg	cca	tgc	caa	cac	aga	tgt	gtg	aat	aca	cac	gga	agc	192
Met	Lys	Pro	Arg	Pro	Cys	Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	
	50					55					60					

tac	aag	tgc	ttt	tgc	ctc	agt	ggc	cac	atg	ctc	atg	cca	gat	gct	acg	240
Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	
65					70					75					80	

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt	288
Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys	
85 90 95	
gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc	336
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu	
100 105 110	
cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc	384
Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala	
115 120 125	
tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt	432
Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe	
130 135 140	
gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc	480
Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile	
145 150 155 160	
agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc	528
Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser	
165 170 175	
cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc	576
His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe	
180 185 190	
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct	624
Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser	
195 200 205	
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc	672
Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr	
210 215 220	
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa	720
Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys	
225 230 235 240	
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct	768
Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro	
245 250 255	
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc	816
Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser	
260 265 270	

aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg	864
Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met	
275 280 285	
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat	912
Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn	
290 295 300	
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg	960
Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val	
305 310 315 320	
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta	1008
Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu	
325 330 335	
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc	1056
Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser	
340 345 350	
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt	1104
Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe	
355 360 365	
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca	1152
Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala	
370 375 380	
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt	1200
Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu	
385 390 395 400	
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat	1248
Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp	
405 410 415	
tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa	1296
Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys	
420 425 430	
aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa	1344
Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu	
435 440 445	
aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc	1392
Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr	
450 455 460	

aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440  
 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu  
 465 470 475 480

atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488  
 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser  
 485 490 495

ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg 1536  
 Leu Leu Ser Val Xaa Xaa  
 500

tatgtcagtt ccttggtttt tttgatattg catcatagga cctctggcat tttaaaatta 1596  
 ctagctgaaa aattg 1611

<210> 3  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 3  
 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro  
 1 5 10 15  
 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe  
 20 25 30  
 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly  
 35 40 45  
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
 50 55 60  
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr  
 65 70 75 80  
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
 85 90 95  
 Glu Asp Thr Glu  
 100

<210> 4  
 <211> 537  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(537)  
 <223> Xaa = Any Amino Acid

<400> 4  
 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro  
 1 5 10 15

Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe  
 20 25 30  
 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly  
 35 40 45  
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser  
 50 55 60  
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr  
 65 70 75 80  
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
 85 90 95  
 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
 100 105 110  
 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala  
 115 120 125  
 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe  
 130 135 140  
 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile  
 145 150 155 160  
 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser  
 165 170 175  
 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe  
 180 185 190  
 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser  
 195 200 205  
 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr  
 210 215 220  
 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys  
 225 230 235 240  
 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro  
 245 250 255  
 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser  
 260 265 270  
 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met  
 275 280 285  
 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn  
 290 295 300  
 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val  
 305 310 315 320  
 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu  
 325 330 335  
 Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser  
 340 345 350  
 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe  
 355 360 365  
 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala  
 370 375 380  
 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu  
 385 390 395 400  
 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp  
 405 410 415

Tyr	Arg	Leu	Ala	Gly	Asp	Lys	Val	Gly	Lys	Leu	Arg	Val	Phe	Val	Lys
			420					425					430		
Asn	Ser	Asn	Ala	Leu	Ala	Trp	Glu	Lys	Thr	Thr	Ser	Glu	Asp	Glu	
		435				440					445				
Lys	Trp	Lys	Thr	Gly	Lys	Ile	Gln	Leu	Tyr	Gln	Gly	Thr	Asp	Ala	Thr
	450				455						460				
Lys	Ser	Ile	Ile	Phe	Glu	Ala	Glu	Arg	Gly	Lys	Gly	Lys	Thr	Gly	Glu
465					470					475					480
Ile	Ala	Val	Asp	Gly	Val	Leu	Leu	Val	Ser	Gly	Leu	Cys	Pro	Asp	Ser
			485						490					495	
Leu	Leu	Ser	Val	Asp	Asp	Xaa	Met	Val	Leu	Ser	Leu	Tyr	Leu	Thr	Leu
			500					505					510		
Tyr	Val	Ser	Ser	Leu	Val	Phe	Leu	Ile	Leu	His	His	Arg	Thr	Ser	Gly
		515					520					525			
Ile	Leu	Lys	Leu	Leu	Ala	Glu	Lys	Leu							
	530					535									

<210> 5  
 <211> 42  
 <212> PRT  
 <213> Drosophila Melanogaster

<220>  
 <221> VARIANT  
 <222> (1)...(42)  
 <223> Xaa = Any Amino Acid

<400> 5  
 Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa  
 1 5 10 15  
 Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe  
 20 25 30  
 Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn  
 35 40

<210> 6  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(39)  
 <223> Xaa = Any Amino Acid

<400> 6  
 Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys  
 1 5 10 15  
 Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa  
 20 25 30

Gly Xaa Xaa Leu Xaa Cys Asp  
35

<210> 7  
<211> 164  
<212> PRT  
<213> Homo sapiens

<400> 7  
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Val Asn  
1 5 10 15  
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr  
20 25 30  
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro  
35 40 45  
Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys  
50 55 60  
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu  
65 70 75 80  
Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys  
85 90 95  
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys  
100 105 110  
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu  
115 120 125  
Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn  
130 135 140  
Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly  
145 150 155 160  
Leu Arg Cys Ser

<210> 8  
<211> 45  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (1)...(45)  
<223> Xaa = Any Amino Acid

<400> 8  
Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa Xaa Cys Xaa Ser Ser Xaa  
1 5 10 15  
Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly  
20 25 30  
Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp  
35 40 45



<210> 9  
 <211> 58  
 <212> PRT  
 <213> Mammalian

<220>  
 <221> VARIANT  
 <222> (1)...(58)  
 <223> Xaa = Any Amino Acid

<400> 9  
 Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His  
 1 5 10 15  
 Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn  
 20 25 30  
 Cys Val Val Gly Tyr Ile Xaa Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln  
 35 40 45  
 Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg  
 50 55

<210> 10  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Exemplary oligonucleotide primer used in sequence  
 assembly process

<221> misc\_feature  
 <222> (8)...(8)  
 <223> n = A, T, C, G, or  
 1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole

<400> 10  
 cctttttntt tttgg

15

<210> 11  
 <211> 15  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Exemplary oligonucleotide primer used in sequence  
 assembly process

<221> misc\_feature  
 <222> (8)...(8)  
 <223> n = A, T, C, G, or  
 1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole

<400> 11  
ccaaaaanaa aaagg

15

<210> 12  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 12  
aaaaaatttt tt

12

<210> 13  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 13  
aaaaattttt ta

12

<210> 14  
<211> 11  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 14  
aaaaattttt t

11

<210> 15  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
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in sequence assembly process

<400> 15

aaaaattttt tc

12

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<213> Artificial Sequence

<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 16

aaaaattttt tg

12

<210> 17  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 17

taaaaatttt tt

12

<210> 18  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 18

caaaaatttt tt

12

<210> 19  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 19

gaaaaatttt tt

12

<210> 20  
<211> 11  
<212> DNA  
<213> Artificial Sequence

*al  
cont.*  
<220>  
<223> Exemplary nucleotide hybridization sequence used  
in sequence assembly process

<400> 20  
aaaaaatttt t

11